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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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11634.333 Million cell updates/sec
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1 ATCTTACATGAACACACAAA.....TGTAAGCACGCACTTCTGAG 2399
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	KEYWORDS	ACCESSION VERSION	DEFINITION	LOCUS	RESULT 1 CRE012098
Kaminski,A.U. and Happe,T. Isolation and characterization of the hydA gene encoding the Fe-hydrogenase of Chlamydomonas reinhardtii	Eukaryota; Viridipiantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas. 1	Chlamydomonas reinhardtii. Chlamydomonas reinhardtii	Fe-hydrogenase; hydA gene.	AJ012098 AJ012098.1 GI:16945125	Chlamydomonas reinhardtii mRNA for Fe-hydrogenase.	CRE012098 2399 bp mRNA linear PLN 15-NOV-2001	

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Best Local Similarity 100.0%;
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2 (bases 1 to 2399)
Happe, T.
Direct Submission
Submitted (15-OCT-1998) Happe T., Molecular Biochemistry, Botanical Institut, Kirschallee 1, D53115-Bonn, GERMANY
Revised by author 31-JAN-2001
Related sequence AJ308413.
                                                                                                             GCCTAGGCAACGTCGCTTGCGCGGCTGCCGCACCCGCTGCGGAGGCGCCTTTGAGTCATG
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/function="hydrogen evolution"
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Chlamydomonas reinhardtii
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Chlamydomonadaceae; Chlamydomonas.
'hames 1 to 2522)
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Chlamydomonas :
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                            CTGCCGCACCCGCTGCGGAGGCGCCTTTGAGTCATGTCCAGCAGGCGCTCGCCGAGCTTG
                                                                                                  GTGTAGCCCTTGCAACACTTGAGGCGCCCGCCACGCCCTAGGCAACGTCGCTTGCGCGG
                                                                                                                    GTGTAGCCCTTGCAACACTTGAGGCGCCCCGCACGCCCTAGGCAACGTCGCTTGCGCGG
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llarity 94.2%;
Conservative
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303..1625
/gene="hydl"
/product="Fe-hydrogenase"
/product="Fe-hydrogenase"
/product="Fe-hydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSALVLKPCAAVSIRGSSCRARQVAPRAPLAASTVRVALATLEA PARKLGNVACAAAPAAEAPKSHVQOALAELAKPKDDPTRKHYCVQVAPAVRVAIAET LGLAPGATTPKQLAEGLERKGFDBVFDTLFGADLTIMEEGSELLHRLTEHLEAHPHSD EPLPMFTSCCPGWIAMLEKSYEPLIPYVSSCKSPQMMLAAMVKSYLAEKKGIAPKDWV MVSIMPCTRKQSEADRDWFCVDADPTLROLDHVITTVELGNIFKERGINLAELPEGEW DNPMGVGSGAGVLFGTTGGVMEAALRTAYELFTGFLFRLSLSEVRGMGIKETMITM VPAPGSKFEELLKHRAAARAEAAAHGTGPGFLAWDGGAGFTSEDGRGGITKIAVAVALGL GNAKKLITKMQAGEAKVDFVEIMACHGTGFCFAGCCGGGQPRSTDKAITQKRQAALYNLDEKSTLRRSHENPSIRELYDTYLGEPLGHKAHELLHTHYVAGGVEEKDEKK"
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/strain="C9"
/db_xref="taxon:3055"
/map="LG III"
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/product="Fe-hydrogenase
/protein_id="AAG00591.1"
/db_xref="GI:9837540"
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/EC_number="1.18.
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135. .1628
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CGCAGAAGCGGCAGGCGGCGCTGTACAACCTGGACGAGAAGTCCACGCTGCGCGCGC	CCTGCCCCGCGGGCTGTGTGGGCGGCGGCGGCCAGCCCGCTCCACCGACAAGGCCATCA	1345 AGAAGCTGATCACCAAGATGCAGGCCGGCGAGGGCCAAGTACGACTTTGTGGAGATCATGG 1404	1285 AGGACGGCAGGGGGGCATCACACTGCGCGTGGCCGTGGCCCAACGGGCTGGGCAACGGCCA 1344	1225 CCGCCGCGACGGCACCCCCGGGCCGGCTGGCCTGGGACGGCGGGCG	1165 CCGCGCCCGGGTCCAAGTTTGAGGAGCTGCTGAAGCACCGCGCGCG	1105 TGAGCCTGAGCGAGGTGCGCGGCATGGACGGCATCAAGGAGACCAACATCACCATCGTGC 1164	1045 TCATGGAGGCGGCGCTGCGCACGGCCTATGAGCTGTTCACGGGCACGCCGCCGCCGCCC 1104		925 AGCTGGGCAACATCTTCAAGGAGCGCGGCATCAACCTGGCCGAGGCTGCCCGAGGGCCAGT 984	865 GGTTCTGTGTGGACGCCGACCCCACCCTGCGCCAGCTGGACCACGTCATCACCACCGTGG 924	805 ACATGGTCATGGTGTCCATCATGCCCTGCACGCGCAAGCAGTCGGAGGCTGACCGCGACT 864	745 TGATGCTGGCGGCCATGGTCAAGTCCTACCTAGCGGAAAAGAAGGGCATCGCGCCCAAAGG 804	685 TGCTGGAGAAATCTTACCCGGACCTGATCCCCTACGTGAGCAGCTGCAAGAGCCCCCAGA 744	625 ACCCGCACTCCGACGAGCCGCTGCCCATGTTCACCAGCTGCTCCCCCGGCTGGATCGCTA 684	565 TGACCATCATGGAGGAGGGCAGCGAGCTGCTGCACCGACCACCCAGGACCACCTGGAGGCCC 624	505 CCGAGGGCCTCCGCCTCGGCTTTGACGAGGTGTTTGACACGCTGTTTGGCGCCGACC 564	445 GTGTCGCTATTGCCGAGACCCTGGGCCTGGGCGCGGGGGGCGCCACCCCCAAGCAGCTGG 504	
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Qy	B 8	B 8	B 8	용성	Db Qy	B 8	B 64	망양	B 6	D &	5	S B &	g Qy	B &	β Q	P 9	B 5	§ §
2398 AG 2399 	2338 CCCTTGGCGCAGCCACGACAGGAGAGGTGTGCATCAGCCGCTTGTAAGCACGCAC	2278 AGAGATGCATTGCAAACGCCTGTAAAAGAACGGCATAGCTACTAGACACTCTGATGTGGA 2337	2218 GCTTTATACCCACCGTATGCGATTGACGTTGGTGTAGGCAACCAGGCGGTAGGAAGGCGG 2277	2158 GCATACGACAACGGGGCCCGTGAGGATTGAGCACTTGACTCGCGAACTTATGAACGTAGC 2217	2098 GGATGCGCACGTTGTGCGCTGGTGGGTGGGCGGGAACGTGGGTAGCATTTAGGCTAGCTG 2157	2038 TTGGTTGGAAGCTAAACATGTTTGGGAACAATTCATCTTACTAAAGCGTGTGGGGGTTGA 2097	1978 TCTGGATATTGAAGCTGCACAAACCTGCATTCTATTTGCTTGTTTACACGTGCCCCAATC 2037	1918 CCTCCAGGGCACGTCGGAATGGCGCGTGCCCATCAACGCAAATTCTTGGCCTTCATCGCT 1977	1858 CTGGCATTAGGCGTAGGTACTGGCATGAGGGAGCGCGGCTTGCTAACCGAATGGCGTATC 1917	AATGO	TGGATAATGCACCGGTGGAGGATTATGGAAGAGGGGGGACTCAGAAGGCTCATTATTGGAC 1	TGTGCGGAGGCCAG	GGTCA GGTCA	1705 TAGCAGTACCGTAAATATGCACTGATGGGTGATGCGGGTGTCCTCTTTATATTGAATGG 1764 	TGAGGAGCGCAGAGGCTCTTTGGGCGGAGACAGCTTCAAAGCGAGGGGGGGTAT 	AGGCGCACGAGCTGCTGCACACCCACTACGTGGCCGGCGGCGTGGAGGACAAGGACGAGA		CGCAGAAGCGGCAGGCGGCGCTGTACAACCTGGACGAGAAGTCCACGCTGCGCGCAGCC 150

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	TGTCGGCGCTCGTGCTGAAGCCCTGCGCGGCGGTGTCTATTCGCGGCAGCTCCTGCAGGG 219	160 TGTCGGCGCTCG	B 8
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TGCGCACGGCCTATGAGCTGTTCACGGGCACGCCGCTGCCGCGCCCTGAGCCTGAGCCAGG	Score 2119.4; DB 8; Length 2454; Pred. No. 9.2e-253; 0; Mismatches 6; Indels 147; Gaps 1;	Query Match 88.3%; Best Local Similarity 93.7%; Matches 2280; Conservative	Que Bes Mat
1000 GCGTGGGCTCGGGCGCCGGCGTGTTCGGCACCACCGGCGGTGTCATGGAGGCGGCGC 1059	GNAKKLITKMQAGEAKYDFVEIMACPAGCVGGGGQPRSTDKAITQKRQAALYNLDEKS TLRRSHENBSIRELYDTYLGEPLGHKAHELLHTHYVAGGVEEKDEKK" 747 c 784 g 430 t Db	GNAKKLI TLRRSHE BASE COUNT 493 a 747 ORIGIN	BASE ORIGI
940 TCAAGGAGCGCGGCATCAACCTGGCCGAGCTGCCCGAGGGGGAGTGGGACAATCCAATGG 999	EPLPMFTSCCPGWIAMLEKSYPDLIPYVSSCKSPQMMLAANVKSYLAEKKGIAPKDMV MVOSIMPCTPRKQSEADRDWFCVDADPTLRQLDBYITTVBLIGNIFKERGINLAELPEGEW DNPMGVGSGAGVLFGTTGGVMEAALRTAYELFGTPLPRLSLSEVRGMDGIKETNITM Db WPAPGSKFEELLKHRAAARAEAAHGTPGPLANDGGAGFTSEDGRGGITLRVAVANGL	Abada Masaw Dubwg Diabada Diabada Diabada Diabada Diabada Diabada Diabada Diabada Diabada Diabada Diabada Diabada	
880 CCGACCCCACCCTGCGCCAGCTGGACCACGTCATCACCACCGTGGAGCTGGGCAACATCT 939	\fightarrow \figh	/db_x/ /tran Parri IGIAP	,
820 CCATCATGCCCTGCACGCGAAGCAGTCGGAGGCTGACCGCGACTGGTTCTGTGTGGACG 879	/gene="hydA"		
760 TGGTCAAGTCCTACCTACCGGAAAGGACGCCACAGGGACATGGTCATGGTGT 819	/clone="Lam9-1"	/clon gene 12 /gene /gene	•
ACCCGGACCTGATCCCCTACGTGAGCAGCTGCAGAGCCCCCAGATGATGCTGGCGGCCA	rdtii"	source 12 /organ /stra /db_x	
AGCCGCTGCCCATGTTCACCACCTGCTGCCCCCGCTGCATCGCTATGCTGGAGAAATCTT	Sciences, National Renewable Energy d, Golden, CO 80401, USA	Direct Sul L Submitted Laborator	TITLE JOURNA FEATURES
580 AGGGCAGCGGCTGCACCGACGACGACGCCTGGAGGCCCACCCGCACTCCGACG 639	QY 2454) Zhang,L., Plummer,S., Ahmann,D., Seibert,M. and Db	FERENCE 2 (bases 1 to AUTHORS Forestier, M.). Ghirardi, M.L.	REFER AUT
	dergoing anaerobiosis		TITLE
	hyceae; Volvocales;		REFER
ACCCCACGCGAAGCACGTCTGCGTGCAGGTGGCTCCGGCCGTTCGTGTCGCTATTGCCG	·	•	ACCESSION VERSION KEYWORDS SOURCE
340 CGGAGGCCCTTTGAGTCATGTCCAGCAGGCGCTCGCCGAGCTTGCCAAGCCCCAAGGACG 399	Qy 2454 bp mRNA linear PLN 31-DEC-2001 Cy reinhardtii iron-hydrogenase HydA (hydA) mRNA, Db	onas	AY055 LOCUS DEFIN
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ACGCCTGTAAAAGAACGGCATAGCTACTAGACA 2325
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                         ACGCCTGTAAAAGAACGGCATAGAAAAAAAAA
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Matches 1030; Conservative
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Prorestier,M., Zhang,L., Plummer,S., Ahmann,
Ghirardi,M.L.
Direct Submission
Submitted (12-SEP-2001) Basic Sciences, Nat
Laboratory, 1617 Cole Boulevard, Golden, CC
Location/Qualifiers
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Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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                                                                               CGAGGGCCTCCGCCTCGGCTTTGACGAGGTGTTTGACACGCTGTTTGGCGCCGACCT
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0; Mismatches 271;
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AJ298228.1 GI:18073434
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'Chlorella' fusca
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LDELAKPKESRLMIAQIASAVRVAIAETIGLAPGDVTIGQLVTGLMNLGFDYVPDTL
FGADLTIMEEGTELLHRLQDHLEQHPMKEEPLDMFTSCCPGWVAMVEKSNPELIPYLS
SCKSPQMMLGAVIKNYX AQVGVOVQPSDICNVSVMFCVRKQGEADREWFNTTGAGLARD
VDHVYTTAEVGKIFLERGIKLMELPESNFDNPIGEGTTGGALLFOTTGGVMEAALRTVY
EVVTQKPMGRVDFEEVRGLEGIKEAEITLKPGDDSPFKAFAGADQGITLKIAVANGL
GNAKKLIKSLSEGKAKYDFIEVMACPGGCIGGGGQPRSTDKQILQKRQQAMYNLDERS
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/product="Fe-hydrogenase"
/EC_number="1.18.99.1"
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/db_xref="taxon:3073"
67._.1377
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/db_xref="GI:18073435"
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 ATGATCTGCTGCACACACTATGTGGCAGGTGGAATTCCAGAGGAGAA
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GWVAMVEKSNPELIPYLSSCKSPQMMLGAVIKNYFAAEAGAKPEDICNVSVMPCVRKS
GEAEPRSGSTMHRAGRRDVDHYMTTAELGKIFVERGIKLMELQESPEDHPVGEGSGGG
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	937. 1317 /note="potential NAD-reducing hydrogenase subunit" /codon_start=1 /codon_start=1 /transI_table=11 /protein_id="haA87055.1" /db_xref="gd:466364" /db_xref="gd:466364" /translation="MSTIRSFEDLKAKROEILDRKAARNGKTIINVSLATCSIAAGGK /translation="MSTIRSFEDLKAKROEILDRKAARNGKTIINVSLATCSIAAGGK /translation="MSTIRSFEDLKAKROEILDRKAARNGKTIINVSLATCSIAAGGK /TEYVNKGEDVEGIIPVNYERVVL" 1330. 1334 1342 2814 /note="potential NAD-reducing hydrogenase subunit"		ង្គីង ប៉ិចិសិជនិទ	DFU07229 Desulfovibrio fructosovorans potential NAD-reducing hydioperon genes, complete cds. U07229 U07229.1 GI:466362 Desulfovibrio fructosovorans Desulfovibrio fructosovorans Desulfovibrio. 1 (bases 1 to 5251) Malki,S., Saimmaime,I., De Luca,G., Rousset,M., Dermoun, Belaich,J.P. Characterization of an operon encoding an NADP-reducing in Desulfovibrio fructosovorans Belatch; J.P. Characterization of fructosovorans Belatch,J.P. Characterization of fructosovorans J. Bacteriol. 177 (10), 2628-2636 (1995) 95270577 7751270

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CTGCGCACCGCCTACGAGCTGGCCACCGGCGAAACCCTTAAGAAGGTCGACTTCGAGGAC
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                                                                                              GGCGCGTCCACGGGCGCGCGCGCGATCTTCGGCGTCACCGGCGGCGTCATCGAGGCGGCG
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INKKAASCRVCVVEVEGERRULAPSCATPVTDMVVKTNSLRVLNARRTVLELLLSDHP
KDCLVCAKSGECELQTLAERFGLIRESPYDGGENSHYKKINSLRVLNARRTVLELLLSDHP
KDCLVCAKSGECELQTLAERFGLIRESPYDGGENSHYKKDISASIIRDMOKCIMCRCE
TMCNTVQTCGVLSGVURGFTAVVAPAFEMNLADTVCTNCGQCVAVCPTGALVEHEYIN
EVVEALANPDKVVIVQTAPAVRAALGEDLGVAPGTSVTGKMAAALRILGFDHVEDTDF
KOVEALANPDKVVIVQTAPAVRAALGEDLGVAPGTSVTGKMAAALRILGFDHVEDTDF
AADLTIMEEGSEFLDRLGKHLAGDTNVKLPILTSCCPGWVKFPEHQFPDMLDVVPSTAK
SPQQMFGAIAKTYYADLLGIBDFDAPLGASTGAAPIFGVTGGVIEAALRTAYELATGE
TRELAKLVKRWNIDPAGLPDEDFDAPLGASTGAAPIFGVTGGVIEAALRTAYELATGE
TLKKVDFEDVRGMDGVKKAKVKVGDNELVIGVAHGLGNARELLKPCGAGETFHAIEVM
ACPGGCIGGGGQPYHHGDVELLKKRTQVLYAEDAGKPLRKSHENPYIIELYEKFLGKP
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/transl_table=11
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Florin,L., Tsokoglou,A. and Happe,T.
A Novel Type of Iron Hydrogenase in the Green Alga Scenedesmus obliquus Is Linked to the Photosynthetic Electron Transport Chain J. Biol. Chem. 276 (9), 6125-6132 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-FEB-2000) Happe T., Nordrhein-Westfalen, Bo
Institute, Universitity Bonn, Karlrobert-Kreiten-Strasse
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AJ271546
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                                                                                                                                                                                                                            /gene="hydA"
1289 . 1463
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                                                                                                                                                                                                                                                                                                                                                   /translation="MPEWQPGGRYAVSVRPPVNRRAVVAAERRRLVVRAAGPTAECDC
ppaparaphyotiofiak pregryndiagiapa avwalaerrrlvvraagptaecdc
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Glamigedyvedtipelak pregryndiagiapa avwalaerplawftscopgwa
MVEKSNPELIPYLSSCKSPQMMLGAVIKNYFAAEAGAKPEDICNVSVMPCVRKOGEAD
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TGGTALAVANGLDERAVIERSHEDLIGALYEKFLGEPNGHKAHELLHTHYVAGGVPDEK"
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2622. .3089,3401. .3877)
/genne="hydA"
/codon_start=1
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1073. .1288
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2622. .3089,3401. .>38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Fe-hydrogenase"
/protein_id="CAC34419.1"
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dA gene for Fe-hydrogenase, exons 1-6.
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                                            DFHYDABG 2887 bp DNA D. fructosovorans hydA and hydB genes. Y11759 Y11759.1 GI:1914863 Fe-hydrogenase; hydA gene; hydB gene; Desulfovibrio fructosovorans. Desulfovibrio fructosovorans
1 (bases 1 to 2887)
Casalot, L., Hatchikian, E.C.,
                          Desulfovibrio.
                                  Bacteria; Proteobacteria;
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2260. .2325
/gene="hydA"
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/gene="hydA"
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/gene="hydA"
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Pred. No. 2.1e-21;
0; Mismatches 144;
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                                    delta subdivision;
 Forget, N.,
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de Philip, P.,
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                                    Desulfovibrionaceae;
                                                                      hydrogenase
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 Belach, J.P.
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Joseph Aiguier, Marseille, 13402 Cedex 09, FRANCE
Location/Qualifiers
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Direct Submission
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Molecular study and partial purification on iron-only hydrogenase in Desulfovibrio fructosovorans
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
CACCACCGAGCATATGCTCACGGGGCTCAAGCAGCTTGGCTTCGACAACGTCTGGGACAA
                                                                                                                                                                                                                                                                                                                        GGCGCTCGCCGAGCTTGCCAAGCCCAAGGACGACGCCCACGCGCAAGCACGTCTGCGTGCA
                                    CACCCCCAAGCAGCTGGCCGAGGGCCTCCGCCTCGGCTTTGACGAGGTGTTTGACAC
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456. 1721
/gene="hydA"
/EC_number="1.12.2.1"
/function="Fe-hydrogenase l
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/gene="hydB"
a 985 c
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/gene="hydB"
/EC_number="1
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/strain="DSM 3604"
/db_xref="taxon:878"
445..1721
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iangkrdaymgestggatifgvsggvmeaalrfayqaltkkppqswdfkavrglngik
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TVLESMNRTTTKFYASLKKRLAL YDAQKA"
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/protein_id="CAA72423.1"
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Pred. No. 4.5e-21;
0; Mismatches 411;
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       1 (bases 1 to 1964)
Voordouw,G., Strang,J.D. a
Organization of the genes
                                                                        D.vulgaris oxamicus (strain Monticello)
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Bacteria; Proteobacteria; delta subdivir
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       . and Wilson, Fee encoding [F
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/transI_table=11
/protein_id="AAR23374.1"
/protein_id="AAR23374.1"
/db_xref="G:145100"
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DRINGVYGADAFPVRASQDNVQVQKLYADFLEKPMSHKAEQLLHTHWVDRSKAIERM
RAQGAYPNPRAKEFEGNTYPYE"
9 a 638 c 633 g 284 t
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CPTGALFGDTGDAHKIPHEBLCINCGQCLTHCCPUGAIYESQSWVTBIEKKIKAKDVKV
IAMPAPAVRYALGDAFGLPVGTVTTGKAFSALKELGFHCWDUSETADVTIWEBGTEF
VORLTKKLDKELPOTTSCCCGCWHKYVESLYPBLFPHMSSCKSPIGMLGTLAKTTYGADR
MKYDRAKVYTVSIMPCTAKKYEGMRPOLWDSGHKDIDATIDTRELAYMIKKAKIDFTK
LPDGKRDTLMGESTGGATLFGVTGGVMEAALRYAYQAVTGKKPESMDFKGVRGLQGVK
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/protein_id="AAA23373.1"
/db_xref="GI:145099"
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                                                                                                                                                                                                                              Data kindly reviewed (17-JAN-1986) by G. Voordouw The put. transcription terminator (pos. 87-105) mapoor expression of the 46-kDa hydrogenase in log. cells transformed with pHVI5.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                Voordouw.G. and Brenner.S.

Nucleotide sequence of the gene encoding Desulfovibrio vulgaris (Hildenborough)

Bur. J. Biochem. 148 (3), 515-520 (1985)
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Desulfovibrio vulgaris
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                                                                                                                                                        /organism="Desulfovibrio vulgaris"
/strain="(Hildenborough)"
/db xref="taxon:881"
/note="inverted repeat A'"
                             note="inverted
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                                                               TACGACCCCAAGCAGGTCTACACCGTCTCCATCATGCCCTGCATCGCAAAGAAGTACGAA
                                                                                        ATCGCGCCAAAGGACATGGTCATGGTGTCCATGCCCTGCACGCGCAAGCAGTCGGAG
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CPTAALIGEMSEPHSIPHIEACINCGCLTHCENAITEACSWYEVEKKEDGKYKC
IAMPAPANKYLALGDAFGMPVGSVTGKWLAALOKLGFAHCMDTEFTADYTIWEEGSEF
VERLTKKSDMPLPQFTSCCPGWQKYAETYYPELLPHFSTCKSPIGMNGALAKTYGAER
MKYDPKQVYTVSIMPCLAKKYEGLRPELKSSCHADIDATLTTRELAYMIKKAGIDFAK
LPDGKRDSLMCESTGGATIFGYTGGYMEAALREAYEAJTGKRPDSWDFKAVRGLDGIK
EATUNVGGTDVKVAVVHGAKRFKQVCDDVKAGKSPYHFIEVMACPGGCVCGGGQPVMP
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/transI_table=1
/protein_id="CAA26267.1"
/brotein_id="CAA26267.1"
/db_xref="GI:40831"
/db_xref="SWISS-PROT:P07603"
/db_xref="SWISS-PROT:P07603"
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DRINGYYGADAKFPVEASQDNTQVKALYKSYLEKPLGHKSHDLLHTHWFDKSKGVKEL
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/note="13.5-kDa protein (aa 1-123)"
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/transl_table=11
/protein_id="CAA26266.1"
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/note="46-kDa hydrogenase
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Institut der Universitaet Bonn, Karlrobert-Kreiten-Str.13, Bonn,
NRW, 53115, GERMANY
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Chlorella fusca hydA gene for Fe-hydrogenase,
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Isolation and molecular characterization of the
from the unicellular green alga Chlorella fusca
Biochim. Biophys. Acta 1576 (3), 330-334 (2002)
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/db_xref="taxon:3073"
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gene="bydA"
/EC_number="1.18.99.1"
/Eunction="hydrogen metabolism"
/codon_start=1
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Best Local Similarity
Matches 246; Conserv
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                                  1594
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1354 TCACCAAGATGCAGGCCGGCGAGGCCAAGTACGACTTTGTGGAGATCATGGCCTGCCCCG
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     AGCTGCTGCACACCCACTACGTGGCCGGCGGCGGCGTGGAGGAGAAGGA 1639
                                                                                                                        CGTCCATCCGCGAGCTGTACGACACGTACCTCGGAGAGACGCCGCTGGGCCACAAGGCGGACA
                                                                                                                                                                                                                                 GGCAGGCGGCGCTGTACAACCTGGACGAGAAGTCCACGCTGCGCCGCAGCACCACGAGAAACC
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                                                                                      CATTCATCCAGGCGCTGTATGACAAGTTCCTAGGCGCACCCCAACAGCCACAAGGCACATG
                                                                                                                                                                                       TCAAGAGCCTGTCAGAGGCCAAGGCCAAGTATGATTTCATTGAGGTCATGGCATGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCAGGGCATCACGCTCAAGATTGCAGTAGCCAATGGGCTTGGCAATGCCAAGAAGCTCA
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1773. .>2246
/gene="hydA"
/number=5
a 803 c
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/EC number="1.18.99.1"
<67. .363</pre>
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/db_xref="GI:21732235"
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gene="hydA"
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/gene="hydA"
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Pred. No. 4e-14;
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Direct Submission

Submitted (15-JAN-1999) Departement de Biologie Moleculaire et Submitted (15-JAN-1999) Tepartement de Biologie Moleculaire et Submitted (15-JAN-1999) Departement de Biologie (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Megasphaera elsdenii putative ÅBC transponcds; and Fe-only hydrogenase (hydA) gene, AF120457. GI:6650983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atta,M. and Meyer,J. Characterization of the gene Megasphaera elsdenii
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Megasphaera elsdenii.
Bacteria; Firmicutes; Clostridia; Clostridiales;
Acidaminococcaceae; Megasphaera.
1 (bases 1 to 2585)
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                                                                   663
                                                                                                                       /Godon_start=1
//transI_table=11
//transI_table=11
//transI_table=11
//produci="ge-only hydrogenase"
/protein_id="AAF22114.1"
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/db xref="GI:665985"
//db xref="GI:665985"
//transIation="MerefreeKIDRRVPIDEHNCAVQFDVTKCKNCTLCRRACADT
//transIation="MerefreeKIVALRRTLGADTVFDTDFGADLTIMEGATELLHRLQ
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PAURVELGEAFENDEGTFVFDLLQHLSGTKSPISILSPUKTYFAQXNIDPK
KIVNVCVTPCTAKKAEIRRPELSASGLFWDEPEIRDTDICITTRELAQWIQDENIDFA
SLEDSKFDKAFGEASGGGRIFGNSGGTWEAAIRTAYHMFTGRPAPKDFIFPFRGLQ
GVKKATUFGHFVLHVAAISGLGNARAFIDDLIKNDAFEDYSFIEVMACFGGGIGGG
QPKVKLPUTFGHFVLHVAAISGLGNARAFIDDLIKNSAFGDYSFIEVMACFGGCIGGGG
QPKVKLPQVKKVQEARTASIYKSDEETDIKASWQNPEIFTLYEAFLDEPLSEMAEFTL
HTYFSDKSDGLGRMKNLTPQTNPMSPKYKPPTEE"
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/strain="ATCC25940"
/db_xref="ATCC:25940"
/db_xref="taxon:907"
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YVQEHGHFVTNQFGQRISATRLLDQFLFFEEMQYTYIAKLSGGERRLYLLRLIMDG
NVLLDEPTBUDLDIPTLTVLERXLDTFQGVVLVVSHDRYFLDRVVDKLFTLEKGTDDR
FYGDYSEYLEEKYSHHQEKKGEKATAPSITKTNITPAKTKAGLTSRQEEELRRITEEL
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/transI_table=11
/product="putative ABC transporter"
/protein_id="AAF22113.1"
/db_xref="GI:6650984"
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/gene="hydA"
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1012, .2466
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98. .1002
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ABC transporter (abc)
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Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.J. McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, I.S., Chardson, Cotton, M.D., Pratt, M.S., Phillips, C.A., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D., Elsen, J.A., Fraser, C.M. et al.
                                                                                                                                                                              Thermotoga maritima. Thermotoga maritima
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nilarity 56.6%;
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of Thermotoga maritima
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Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchun, K.A., McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D., White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M.
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INPEHLLIGI LREGEGIATHI LRKLIGUDI ATLEREI IDIYSYSSKKALEYEEEEDYTY
RSVKQLEGFGVNLTELAAKKELDPVIGREEEIRENKYQVLYRKKKANPVLIGDEGVGKT
AIVEGLAGRIVAGDVPEILMYKVIFSLDVAALVAGTKYRGEFEEKHKKKLLQYTKKDKN
ILFIDETHTIVGAGSAEGAIDAANILKPALARGEISCIGATTPDEYRRYIEKDAALE
RRFOKIYVKEPTEEETLEILKGLKRYKEAHKVIYTDKALEAVYLSKRYITDHYLPD
KAIDVIDEAGARARLKVFVLPPELKDMKLELERIRSKELAVUNQDVEKAAQUKEEEM
BLEAEYRKRYAEMRERSVSLIGAPGVYGVEGGTITEKVRRFEEKLLNLEEA
LHQRIVAGDEAIKAVARAERRREGEIGKUDRRFIGVFLFLEFTGVGKKTELAKALAEYLF
GDERALIREDMSEKMERESVSLLIGAPGGVYGYEEGGTITEKVRRFFSVILFDEIEK
AHPDVFNILLQIMDDGRLTDSQGREVDFRNTIIIMTSNIGSSYINKSKRTLGGVGDNN
EEKSFEKIKOLVLEEVKRTFREBEINRIDETLIFHPLKKEHEGIIDILLERDLRKRLS
EEKSFEKIKOLVLEEVKRTFREBEINRIDETLIFHPLKKEHEGIIDILLERDLRKRLS
EEKSPEKIKOLVLEEVKRTFREBEINRIDETLIFHPLKKEHEGIIDILLERDLRKRLS
                                                                                                                                                                                                                                                                                                         /translation="MKKFVCSNCGYVSPKWFGRCPQCGEYDTAEEVQRRKNREGSPSL
FUNLEDAGEISLERLSTGFSELDRAFRGGIVPGQVILLSGEPGIGKSTIALDIAERFA
ERGLVVYVSGEESPQOLKLRADRILLKERKDILLTLENDIEIISSLONKRVSFMVVD
SIQTVFSSDLGSSPGSISQVKRVTMKTIDFAKKRGVPVLLVGHVTKSGEIAGPKLVEH
MYDTVAXFEGDRRTGLRLLKITKNRFGPSDEVAVFELKENGFVQYENPSFTBGDADLD
GNVLTCVFEGTKPFVVGIQALVSKNRTFSPKRVCKGVDVNRVMLLIAVISKYLKLPIE
THDVYVNVVGGLRVTDPAADLAIALSIVSSYLEVSLHNTAAVGEIGLDGRVRKVYNIN
RRLNSLKSSGRIIVPPIEEEQKGVFEVRDLKEAVSIIGGEILGTPGAD"
                                                                                          /note="similar to GB:D26185 SP:P37573 GB:AL009126 percent identity: 65.12; sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /notes"similar to Sp. P24554 GB. X63155 PID: 537229 PID: 581233 GB: U00096 percent identity: 63.78; ide by sequence similarity; putative" /codon start=1 /codon start=1
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product="conserved hypothetical protein"
                                           /codon_start=1
/transl_table=
                                                                                                                                                                                                                                  /gene="TM0200"
}883. .4956
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/protein_id="AAD35291.1"
/db_xref="GI:4980696"
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/product="ATP-dependent Clp protease, ATPase subunit"
/protein id="AAD35290.1"
/db_xref="GI:4980695"
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db_xref="taxon:2336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MFDKFSEKTAQIFVTAQEEAKELGHSYVGTEHLLLAILKVDRSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="TM0198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                  4956
                                           table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TM0198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TM0199"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  maritima"
                                                                                                                                                            PID:467476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identified
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/gene="TM0201"
/note="similar to (
69.31; identified h
/codon start=1
/transi_table=11
                                                                                                                                                                                                                                                    8452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="TM0203"
7745. .8476
/gene="TM0203"
                                                                                                                                                       8452. .9153
/gene="TM0204"
                                                                                                                                                                                                                                                                                            /translation="mravegillvliawyllhflepsslilpgpvetekvfikmlnre
Teballstllkglvstfiviavglpvgffmgisdrvyeflrplvtvvqavpvvsmlvv
Viflwgigwqgpvvisslslipvaifttvsgvrsvdrkllevmkvyrvprrmilkevy
LGSImpfvlsilevssgnvmkavvmebylcgdsglgvlismarqyvdvprvyaltift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITVIEACEKAGIEIPALCHHPRIGESIGACRVCVVEVEGARNIQPACVTKVRDGMVIK
TSSDRVKTARKENLALLLSEHPNDCMTCEANGRCEFODLI YKYDVEBIFGYGTKEGLV
DRSSPAIVRDLSKCIKOGNCVRACSELOGMHIYSMVERGHRTYPGTPEDMPVYETDCI
GCGQCAAFCPTGAIVENSAVKVVLEELLEKKEKILVVQTAPSVRVAIGEEFGYAPGTIS
TOGMVAALRRIGFDYVFDTNGGADLTIMEBGSEFLERLEKGDLEDLPMFTSCCPGWVN
LVEKVYPELRTRLSSAKSPQGMLSAMWKTYFALKLGVKFEDIFHVSIMPCTAKKDEAL
RKQLMVNGVPADVULTTRELGKLIRMKKIPFANLFBEETDAPLGISTGAAALFGVTG
GVMEAALRTAYELKTGKALPKIVFEEVRGLKGVREAEIDLDGKKIRIAVVHGTANVRN
LVEKLIRREVKKHFVEVMACPGGCIGGGQQPYSRDPBILRKBAEAITTIDERMTLRKS
/codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="TM0202"
6846. .7748
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/db_xref="G1:4980697"
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LEKYKDNFNKLLSELBVLELENRVTLADVVRTLAKGFELRIFIVEEIRPYIVELGEEGR
LARMOLRELTEDVDDLLVLLIMDYSSEEVEEETAQNIIQDFITRREPSDISISRVLGY
DVQQAAQLDVLVSARGYRLLKTVARIPLSIGYNVVRMFKTLDQISKASVEDLKKVEG
                                                                                            dentified by sequence similarity;
                                                                                                                                                                                                                                                                          /VLGISFERSVKVLARRVWKKWRLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7745. .8476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6846. .7748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HENPAIKKLYEEYLEHPLSHKAHELLHTYYEDRSRKKRLAVK"
                                                                                                                                                                                                                  gene="TM0204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="similar to PID:2440148 percent identity:
dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical
/protein_id="AAD35294.1
/db_xref="GI:4980699"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence similarity;
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/gene="TM0202"
                                                                                      note="similar to GB:AE000782 percent identity: 68.28; dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1/
transI_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="NADP-reducing hydrogenase, subunit D,
/protein_id="AAD35293.1"
/db_xref="G1:4980698"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MRRFFKNNLRNLSQNGETNSVRRCFALADVTVVINGRTLTVPDN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="TM0201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEKRARAISESISSLKHRKTSE"
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Query Match
Best Local Similarity
Matches 402; Conserv
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                                                                                                                                                                                                                                                                               771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGTTCACCAGCTGCTGCCCCGGCTGGATCGCTATGCTGGAGAAATCTTACCCCGGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCTGCACCGCCTCACCGAGCACCTGGAGGCCCACCCGCACTCCGACGAGCCGCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGCGCCGGGCGCCACCACCCCCAAGCAGCTGGCCGAGGGCCTCCGCCTCCGCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCACGTCTGCGTGCAGGTGGCTCCGGCCGTTCGTGTCGCTATTGCCGAGACCCCTGGGC
                                                                               reca cececa a en ceca a en cece ce a creer recener en cece ca en cece a 
                                                                                                                                                                                                                                                                               TACCTAGCGGAAAAGAAGGGCATCGCGCCAAAGGACATGGTCATGGTGTCCATCATGCCC
                                                                                                                                                                                                                                                                                                                                                                             AGAACGAGGCTTTCCTCTGCCAAGTCTCCACAGGGAATGCTCTCCGCTATGGTGAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCCCCTACGTGAGCAGCTGCAAGAGCCCCCAGATGATGCTGGCGGCCATGGTCAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTTCACTTCTTGTTGTCCTGGTTGGGTGAACCTTGTGGAAAAGGTCTATCCCGAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCTCGAAAGACT-----
TGTACCGCGAAGAAGGACGAGGCTCTGAGAAAACAGCTCATGGTGAACGGTGTTCCAGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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LLKELDDPLLENKDLEEKLQAFLDYVKEIPNLPEARKEYRIGKSLEMIEKLRSWFLID
YLECGGEGEVDLSTD.OYAKGVGEPNRKKKLKKIGIETLADLLEFFENDYEDRRKIFEKLR
DLLPGEKVTTQGKIVSVETKKFQNMNILTAVLSDGLVHVPLKWFNQDYLQTYLKQLTG
KEVFVTGTVKSNAYTQQYEINHAEVTPKLGEGEVRRILPTRLTSGISQKQMRKIFEN
IPSLCCSLKETLPERLLEKKRLLGVKDAYYQMHEPKTTFYHLEKARERLAYEELFVLQL
AFQKIRKEREKHGGIPKKIEGKLAEEFIKSLPFKLTNAQKRAHQEIRNDMISEKPMNR
LLQGDVGSGKTVVAQLAILDNYEAGFQTAFMVPTSILAIQHYRRTVESFSKFNIHVAL
LIGATTPSEKEKIKSGLRNGQIDVVIGTHALIQEDVHFKNLGLVIIDDGHRFGVKQRE
ALMNKGKMVDTTLVMSATFIPRSMALAFYGDLDVTVIDEMPFGRKEVQTMLVPMDRVNE
VYEEVRQEVMRGGQAFIVYBLLEESDKLNVKSAVEMYEYLSKEVPFPEKLGLMHGRKS
QEEKDRWMLEFAEGRYDILVSTTVIEVGIDVPRANVMVIENPERFGLAQLHQLRGRVG
RGGGDAYCFLVVGDVGEAMBELRFFTLNTDGFKIAEYDLKTRGPGEFFGVKQHGLSG
RKGADLYRDLKLLEMAREDVOEIDVEGIELPEEIKLIEVG"
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GKTTFLRIVSGLEDYQGKVKVFTDKIGYVFQEPRLIPWKTITENLMLIRRDTDRIASL
LEKVELKGFENHYPWQLSEGMKQRVNFVRALLVDPDLLLLDEPFDALDLKTKMKVMDL
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RLEKMVIERLLNLLR"
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/gene="TM0206"
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/gene="TM0206"
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/db_xref="GI:4980701"
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/db_xref="GI:4980702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="ATP-dependent DNA helicase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="similar to GP:2633959 percent identity:
dentified by sequence similarity; putative"
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54.1%;
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Pred. No. 7.2e-12;
0; Mismatches 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---CGAAAAAGGCGACCTTGAAGACCTCCCC
                                                                                                                                                                                           CATTTTCCACGT
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AUTHORS
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Submitted (15-JAN-1991) J.P.W.G. Stokkermans,
Wageningen, Dept of Biochemistry, Dreijenlaan
Wageningen, The Netherlands
2 (bases 1 to 1940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hyd Gamma, a gene from Desulfovibrio vulgaris (Hidenborough) encodes a polypeptide homologous to the periplasmic hydrogen FEMS Microbiol. Lett. 58, 217-222 (1989)
Data kindly reviewed (14-MAR-1991) by Stokkermans J.
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Best Local Similarity 52.3%;
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                                CGCGCGCCGAGGCCGCCGCG 1232
                                                                                                                                                                                  GCCGCTGCCGCCTGAGCCTGAGCGAGGTGCGCGCATGGACGGCATCAAGGAGACCAA 1150
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Search completed: June 8, 2003, 11:53:21 Job time : 6045 secs

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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match Length DB	1 DB	ID	Description
_	93	3.9 1737	20	AAZ25199	Clostridium pasteu
c 2	83.2	3.5 114955		AAX53491	Human adenosine Al
w	75	3.1 109519	22	AAS08693	Micromonospora DNA
4.	72.6	3.0 114955	20	AAX53491	Human adenosine Al
5	71.4	3.0 1562	22	AAH13714	Human cDNA sequenc
σ	71.4	3.0 1577	22	AAH27127	Human NADP hydroge
7	70.2	2.9 65140	22	AAD17184	Streptomyces nours
8	70.2	2.9 125401	. 22	AAD17186	Streptomyces nours
9	69.8	2.9 1836	21	AAA70438	HIV gp140.mut.modS

45 63.4	44 63.4	0		63.	63.	63.	o.	65.	65.	67.	67.	67.	67.	67.	67.	68.	68.	69.		69.	69.	69.	69.	69.	69.	69.	69.	69.	69.	69.	69.	13 69.8	69.	69.	
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AAV11297	AAD14507	\BL39983	AA51951	VAA51959	AAQ15153	AAQ14478	AAA09469	AT80414	AT78508	\BL39955	AAA51615	AAA51614	AAC91328	AAH24245	AAA51613	AAV21187	ABL40024	AD17185	AAA70471	AAA70473	AAA70445	AAA70446	AAA51966	AAA70447	AAA51948	AAA51947	AAA51946	AAA51949	AAA51945	AAA51944	AAA70436	AAA70433	AAA70437	AAA70435	AAA70434
Nucleotide sequenc	gerı	Synthetic Pol poly	-\ -\	Modified HIV-1 Env	Swine herpes virus	gene.	Streptococcus olea	Platenolide syntha	Platenolide syntha	Synthetic Env poly	HIV gp160 with sig	HIV gp160 coding r	Human polynucleoti	Human oxidoreducta	HIV gp140 coding r	Amycolatopsis medi	Synthetic Pol poly	Streptomyces nours	HIV bicistronic co	HIV bicistronic co	HIV gp160.modSF162	HIV gp160.modSF162	Modified HIV-1 Env	0.modSF	HIV-1	HIV-1	HIV-1	1-AIH	HIV-1	-	HIV gp140.mut.modS	gp140	gp140	gp140	gp140.mods

ALIGNMENTS

199 AAZ25199 standard; DNA; 1737 BP. AAZ25199; 13-DEC-1999 (first entry) Clostridium pasteurianum hydrogenase #2. Clostridium; hydrogenase; blue-green alga; hydrogen; microbe; Shine-Dalgarno; ss. Clostridium pasteurianum.					×	DT 13	×		×		AAZ25199	RESULT 1
	lostridium pasteurianum.	hine-Dalgarno; ss.	lostridium; hydrogenase; blue-green alga; hydrogen; microbe;	lostridium pasteurianum hydrogenase #2.		13-DEC-1999 (first entry)		AAZ25199;		AAZ25199 standard; DNA; 1737 BP	99	

PR XXX PR 13-MAR-1998; 13-MAR-1998; 21-SEP-1999. JP11253166-A 98JP-0062601. 98JP-0062601.

(AGEN) AGENCY OF IND SCI & TECHNOLOGY.

WPI; 1999-583699/50.

Preparation of heterologous hydrogenase in blue-green algae for production of hydrogen and is environmentally friendly Example 4; Fig 10; 12pp; Japanese.

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A method has been developed for the preparation of hydrogenase in which a blue-green alga introduced by a recombinant vector containing a cheterologous hydrogenase gene is cultured in a medium to form and accumulate hydrogenase in the microbe body. Also claimed are: (1) a blue-green alga introduced by a recombinant vector containing a gene having a Shine-Dalgarno sequence consisting of AAGGAA upstream of the hydrogenase structural gene derived from a Clostridium genus microbe; (2) a method for the production of hydrogen by culturing the above blue-green alga under light irradiation; (3) a method for the production of hydrogen by reacting the above blue-green alga anaerobically and then under light irradiation; (4) a method for the production of thydrogen by reacting the above blue-green alga with an electron receptor; and (5) a method for the production of hydrogen by reacting the above blue-green alga with an electron receptor. The method is mild to environment. The present sequence represents a Clostridium pasteurianum hydrogenase mucleotide sequence from an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 359;
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Similarity 48.1%;
59; Conservative
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TCTGCGGAGTGCAAAAGACTTTGCTGAAAACGCTGAACTTGAAGATATCGAATATAAGCA
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Pred. No. 1.1e-07;
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Query Match Best Local Similarity

3.5%; 31.5%;

Score 83.2; Pred. No. 7

DB 20;

Length 114955

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RESULT 2
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ID AAX534
XX AAX54
XX AAX5
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                                                                                            The specification describes antisense oligonucleotides (AAX52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and con-coding regions of RNAs corresponding to target genes, gene coding regions, genemic flanking regions, intron-exon borders, the intrinction codons, genemic flanking regions, intron-exon borders, the creations and all segments of RNAs encoding proteins associated with one coding and anon-coding regions and all segments of RNAs encoding proteins associated with one compared to the conditions or mixtures. The antisense oligonucleotides (specifically AAX5510-71) can be used for the coding only be derived from sequences AAX5510-71) can be used for the coding only conditions are those associated with impaired respiration and conditions are those associated with impaired respiration and conditions are those associated with impaired respiration, including lung diseases, pulmonary vasoconstriction, codinflammation, including lung diseases, pulmonary vasoconstriction, coding number of conditions are those associated with impaired respiration and conditions are those associated with impaired respiration and conditions are those associated with impaired respiration and conditions.

CC inflammation, including lung diseases, pulmonary vasoconstriction, caphysema, chronic codes conditions of the pulmonary disease (colon cancer such as luxhemias, colon cancer, breast cancer, lung cancer, cor panceratic cancer, hepatocellular carcinoma, kidney cancer, melanoma, bepatic metastasize, as well as all types of cancers which may metastasize to the lungs including breast and prograte cancer.
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17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 37; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides used in treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1998;
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97US-0059160.
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   6071 A;
   29417 C;
                                                                             lungs, including breast and
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       36712 G;
   21328 T;
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   21427 other;
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The specification describes antisense oligonucleotides (AAX52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and conn-coding regions of RNAs corresponding to target genes, gene coding regions, gene militation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one cor more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target coligonucleotides (specifically AAX55180-271) can be used for the coligonuc
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Pred. No. 0.
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ed. No. 0.00058;
Mismatches 742;
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                                                        therapy;
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29-JUL-1999; 27-AUG-1999; 11-JAN-2000; 02-MAY-2000; 09-JUN-2000; 28-JUL-2000; 99JP-0248036. 99JP-0300253. 2000JP-0118776. 2000JP-0183767. 2000JP-0241899. 2000EP-0116126

Ota T, Ishii Ś Isogai T, ;, Sugiyama Nishikawa T, T, Wakamatsu Hayashi A, Naga ashi K, Nagai F ~ Saito K, Otsuki

HELIX RES

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs detection by the

8; SEQ ID 10601; 2537pp + 8 ROM; English S

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination combination

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RRSULT 6
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Matches 159; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 1 send sequence, where the combination of oligonucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                       disease; inflammation;
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                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                     "NADP hydrogenase subunit
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Pred. No. 0.00075
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RESULT 7
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Best Local Similarity
Matches 159; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to NADP hydrogenase subunit 50. Included in the invention are nucleotide and amino acid sequences for NADP hydrogenase 50 subunit, a vector containing the cDNA sequence, a host cell transformed with the vector, and an antibody directed against the protein. The polypeptide and polynucleotide can be used in the diagnosis and treatment of cancer, haemopathy, HIV infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADP hydrogenase subunit 50 and encoded polynucleotide, applicable in diagnosis and treatment of cancer, hemopathy, HIV infection, immunological diseases and inflammation -
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 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-300475/31.
P-PSDB; AAB97260.
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                                              Streptomyces
                                                                                                                       Streptomyces noursei nysl DNA of nystatin PKS
                                                                                                                                                     29-NOV-2001
                                                                                                                                                                                   AAD17184;
                                                                                            Polyketide
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                                                                                                                                                                                                                                                                                                                        ACTAC
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                                                                                                                                                                                                                                                                                            CGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGCATTTACGCTGACATCCCTGTGCGGCGTCCGGAGTCCAGTGCACACGTGCAGGAGC
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                                                                          synthase; PK; antibiotic;
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                                               noursei.
                                                                                                                                                     (first entry)
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Location/Qualifiers complement (1..1035)
                                                                                                                                                                                                                DNA; 65140
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                                                                         PKS; macrolide; nystatin; ic; nys1; ds.
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Pred. No. 0.00075;
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                                                                                                                       gene cluster.
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          WPI; 2001-557614/62.
P-PSDB; AAE10125, AAE10126, AAE10127, AAE10128, AAE10129, AAE10130,
AAE10131, AAE10132, AAE10133, AAE10134, AAE10135, AAE10136, AAE101
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10-APR-2000; 2000GB-0008786.
14-APR-2000; 2000GB-0009387.
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                                                                             (ZOTC/)
(SEKU/)
(FJAE/)
(BRAU/)
                                                                                                                   (SINY-)
                                                                                                                                                                                          08-FEB-2001; 2001WO-GB00509
                                                                                                                                                                                                                          WO200159126-A2
                                                                                                             (DZIE/)
nystatin polyketide synthase polynucleotides and polypeptides,
                                       / SB, Senc.
S. Ellingsen 7
                                                                    ALPHARMA AS.
SINVEMSKA H.
DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
STROM A R.
                                                                                                                                    UNIV NORGES TEKNISK NATURVITENSKAPELIGE. SINTEF STIFTELSEN IND TEK FORSK.
                                             Sekurova ON,
lingsen TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "NysD2 partial protein"
/note= "CDS does not include stop
complement (1056..2576)
                                                                                                                                                                                                                                                        /product= "ORF2 protein"
/note= "CDS does not inc
63765..64961
                                                                                                                                                                                                                                                                                       /product= "NysR5 protein"
/note= "CDS does not include
complement (62551..63615)
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                                                                                                                                                                                                                                          /product= "ORF1 protein'
                                                                                                                                                                                                                                                                                                                              products "NysR4 (short) protein"
                                                                                                                                                                                                                                                                                                                                                    0415..61047
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6550..49840
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note= "CDS does
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Sletta H,
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Best Local Sim:
Matches 573;
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 CGCTGCGCACGGCCTATGAGCTGTTCACGGGCACGCCGCTGCCGCCCTGAGCCTGAGCG 1116
                                                                                                             CGGGACTGGGCGCCGACCACCCGCTGCTCGGCGCCACCGTCGAACTCGCCGACGGGG
                         TGGGCGTGGGCTCGGGCGCGGCGGCGGTGTCATGGAGGCGG
                                                CCTTCCAGCACCAGCGGTTCTGGCCGACCGCGGCCGCCCCAGGACGTCACCGCCG
                                                              ACGCCGACCCCACCCTGCGCCAGCTGGACCACGTCATCACCACCGTGGAGCTGGGCAACA 936
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The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a Streptomyces noursei nysl DNA of nystatin PKS gene cl
                                                                                                                                                                                                                                    Page 116-151; 266pp; English.
                                                                                                                                                                                                                                                                            antibiotics and
    Conservative
                    2.9%;
                                                                            8270 A; 25171 C;
                                                                                                                                                                                                                                                                          antifungals
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Score 70.2; DB 2
Pred. No. 0.0015;
0; Mismatches 75
                                                                              22273 G; 9426
                                      DB 22;
    758;
    Indels
                                      Length
                                                                              T; 0 other;
                                          65140
    18;
    Gaps
                                                                                                                         cluster.
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AGGCGCCGCCACGCCTAGGCAACGTCGCTTGCGCGGCTGCCGCACCCGCTGCGGAGG GCTTTGACGAGGTGTTTG-----ACACGCTGTTTGGCGCCGACCTGACCATCATGGAGG GGCCCACCTCCGTCGTCGTCGCCGGCACCGAGGAAGCCGTCGCCGCGATCGGGGGCGCGCT CGCGCAAGCACGTCTGCGTGCAGGTGGCTCCGGCCGTTCGTCGCTATTGCCGAGACCC CCGCCCGCGCCCCCCCATGCAGGCCCCTGCCGCGCGGCGGCGCGATGCTCGCGATCCGCG TGTCCATCATGCCCTGCACGCGCAAGCAGTCGGAGGCTGACCGCGACTGGTTCTGTGTGG CCATGGCCCAGGAATCCCTGCCGGACGGCGCCGCCGCCGTGCCGCTGCTGCGCAAGGACC 19055 CCATGGTCAAGTCCTACCTAGCGGAAAAGAAGGGCATCGCGCGAAAGGACATGGTCATGG CCCTCACCGACCGCGGCGTGACCACGCTCGTCGAACTCGGCCCGGACGGCGTGCTGTCCG CTTACCCGGACCTGATCCCCTACGTGAGCAGCTGCAAGAGCCCCCAGATGATGCTGGCGG CCGCCGACTACTGGGTCCGCCACGTCCGCGAGGCGGTCCGCTTCGCCGACGGCGTCACCG AGCCGCTGCCCATGTTCACCAGCTGCTGC---CCCGGCTGGATCGCTATGCTGGAGAAAT CGCGCATCCCGGTCCTCTCCAACCTCACCGGCACCGTCGCCGCCGTCGCCGACCTGTGCT AGGGCAGCGAGCTGCTCACCGCCTCACCGAGCACCTGGAGGCCCACCGCCACTCCGACG TCATGGACCCGATGCTGGCGGAATTCCGCGCGCGCGCGGGCCTGACCTACCACGAGC TCACCGCCCAGGACCGCAAGACCACCGGCTGCGGGTCAGCCACGCCTTCCACTCGCCGC тевесствесессеевсесках сесссамесь в тевессем в постое в тересе в те CCACCGAGGACGÁGGTCACCCCCCACCTCACCGÁCGACGTCTCGATCGCCGCCGTCAACG CGCCTTTGAGTCATGTCCAGCAGGCGCTCGCCGAGCTTGCCAAGCCCAAGGACGACCCCA AGCTCGCCGCCGCGCACGTCGCCGGGGTCCTCTCCCTCGAAGACGCCTGCACCCTCGTCG 579 18695 696 639 525 405 18515 285 756 18815 18755 465 18635 18575 345 876 816 18935 18995

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RESULT 8
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/note= "CDS does not include
complement (59045..60241)
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complement (58786..58980)
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6337..34771
/product= "NysN protein"
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complement (60238..61296)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valla
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(SINV-)
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DZIEGLEWSKA H.
ZOTCHEV S B.
ZOTCHEV O N.
SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
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Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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01-DEC-1999;
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The present invention relates to synthetic HIV protein expression cassettes. The present sequence is the coding sequence of a synthetic HIV Env expression cassette. In, addition, synthetic HIV Gas expression cassettes have been constructed. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes of the present invention may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).

Sequence 1836 BP; 414 A; 623 C; 550 G; 249 T; 0 other;

밁 Query Match 2.9%; Best Local Similarity 44.3%; Matches 422; Conservative 784 GCCCACTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACCAAG CCGGACCTGATCCCCTACGTGAGCAGCTGCAAGAGCCCCCAGATGATGCTGGCGGCCATG CTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCAACAACAACACCCCGCAAGAGCATC GAGGGCGTGGTGATCCGCAGCAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAG CTCGGCTTTGACGAGGTGTTTGACACGCTGTTTTGGCGCCGACCTGACCATCATGGAGGAG ACCCTGGGCCTGGCCGGGCCCACCACCACCCAAGCAGCTGGCCGAGGGCCTCCGCCGC ACCATCGGCCCGGCCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAG CCGCTGCCCATGTTCACCAGCTGCTGCCCCGGCTGGATCGCTATGCTGGAGAAATCTTAC GGCAGCGAGCTGCTGCACCGCCTCACCGAGCACCTGGAGGCCCACCCGCACTCCGACGAG <u>.</u>. Score 69.8; DB 2 Pred. No. 0.0015; 0; Mismatches 52 DB 21; 522; Indels Length 1836; و آ Gaps 761 603 701 641 663 581 521 783 ω

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Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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Claim 19; Fig 24; 391pp; English

The present invention relates to synthetic HIV protein expression cassettes. The present sequence is the coding sequence of a synthetic HIV Env expression cassette. In, addition, synthetic HIV Gag expression cassettes have been constructed. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes of the present invention may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired mmunodeficiency syndrome (AIDS).

Sequence 1944 BP; 450 A; 656 C; 577 G; 261 T; 0 other;

Query Match Best Local S Matches 422

Similarity

2.9%;

Score 69.8; Pred. No. 0. Mismatches

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                     The present invention relates to synthetic HIV protein expression cassettes. The present sequence is the coding sequence of a synthetic HIV Env expression cassette. In, addition, synthetic HIV Gag expression cassettes have been constructed. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes of the present invention may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
                                                                                                                                                                                                                           Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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01-DEC-1999;
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RESULT 12
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DT 28-NO AAA70437; AAA70437 standard; DNA;

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Query Match 2.9%; Best Local Similarity 44.3%; Matches 422; Conservative

Score 69.8; DB 2 Pred. No. 0.0015; 0; Mismatches 52

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28-NOV-2000

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Sequence 1944 BP;

450 A; 656 C; 577 G;

261 T; 0 DB 21;

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Best Local Similarity
Matches 422; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnett S, Zur
Greer C, Selby
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1944 BP; 451 A; 655 C; 577 G;
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01-DEC-1999;
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                                                         GTCAAGTCCTACCTAGCGGAAAAGAAGGGCATCGCGCCAAAGGACATGGTCATGGTGTCC
                                                                                     GCCCACTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGCAGATCGTGACCAAG
                                                                                                         CCGGACCTGATCCCCTACGTGAGCAGCTGCAAGAGCCCCCAGATGATGCTGGCGGCCATG
                                                                                                                                                                            CCGCTGCCCATGTTCACCAGCTGCTGCCCCGGCTGGATCGCTATGCTGGAGAAATCTTAC
                                                                                                                                                                                                                                                                                                CTCGGCTTTGACGAGGTGTTTGACACGCTGTTTGGCGCCGACCTGACCATCATGGAGGAG
ATCATGCCCTGCACGCGAAGCAGTCGGAGGCTGACCGCGACTGGTTCTGTGTGGACGCC
                             CTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCC
                                                                                                                                                ACCATCGGCCCCGGCCGCCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAG
                                                                                                                                                                                                          CTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCCAACAACAACACCCCGCAAGAGCATC
                                                                                                                                                                                                                                                                                                                             ACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAG
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M, Walker
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RESULT 13
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                        Barnett Greer C,
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01-DEC-1999;
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                                                                                                                                                                                                                                                                                            HIV gp140.modSF162 construct coding sequence
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WPI; 2000-452400/39
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                                                                 (CHIR ) CHIRON
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Expression cassettes encoding the Gag-containing polypeptide useful

human immunodeficiency virus for vaccinating against HIV

(VIV)

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Query Match
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GGCGTGGCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACC 1512
                                                                                                  ATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTG
                                                                                                                                                GTGCGCGCATGGACGCATCAAGGAGACCAACATCACCATGGT---GCCCGCGCCCGGG 1175
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Pred. No. 0.
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Matches
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Best Local
                                                                                              The present invention relates to synthetic HIV protein expression cassettes. The present sequence is the coding sequence of a synthetic HIV Env expression cassette. In, addition, synthetic HIV Gag expression cassettes have been constructed. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in, viral replication. The expression cassettes of the present invention may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired
                                                                                                                                                                                                                                                                                  Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                                                                                                                                                                                                                                                                                        Barnett S, Zur
Greer C, Selby
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01-DEC-1999;
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                                                                                     immunodeficiency syndrome (AIDS).
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HIV-1; vaccine; anti-HIV; immunogenic; modified; envelope; CD4 binding region; V1/V2 loop; bridging sheet; ss.
                                                                                          31-OCT-2000
                                                    Modified HIV-1 Env gp160, Val120-Ala204
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Synthetic.
                                                               WO200039303-A2
                                                                    Human immunodeficiency virus type 1 isolate SF162
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06-JUL-2000.

30-DEC-1999; 99WO-US31272

31-DEC-1998; 29-SEP-1999; 98US-0114495 99US-0156670

(CHIR) CHIRON CORP

Barnett S, Hartog K, Martin m

2000-465745/40.

Novel modified HIV Env preparing a vaccine to of HIV subtypes polypeptides useful as immunizing agents and elicit an immune response against a broad ran

Claim 14; Page 118; 139pp; English.

first composition comprising a polynucleotide encoding the Env polypeptide in a priming step and administering a second composition comprising a modified Env polypeptide as a booster in an amount sufficient to induce an immune response in the individual. The first and/or second composition further comprises an adjuvant (claimed). The intracellularly produced Env polypeptides can be used for a number of diagnostic and therapeutic purposes to determine the presence of reactive antibodies/and or Env proteins in a biological sample to aid in the diagnosts of HIV infection or disease status or as measure of response to Novel immunogenic modified human immunodeficiency virus (HIV) envelope (Env) polypeptides having an amino acid deleted or replaced in the region corresponding to residues 420-436 or 119-123 and 199-210 relative to isolate HXB-2 are disclosed. The modified Env polypeptide is based on HIV strain SF162, with numbering relative to isolate HXB-2. The Env polypeptides are modified so as to expose at least part of the CD4 binding region. The modified HIV Env polypeptides, coding polypucleotides and constructs, further comprising an adjuvant, are used for inducing an immune response in an individual. The method involves administering a

Sequence 2310 BP; 477 A; 805 ü 707 G; 321 T; 0 other;

Query Match Best Local

Similarity

2.9%;

0015

DB 21; Length

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762 GTCAAGTCCTACCTAGCGGAAAAGAAGGGCATCGCGCCAAAGGACATGGTCATGGTGTCCC
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                                                                       GCCCÁCTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACCAAG
                                                                                                                 CCGGACCTGATCCCCTACGTGAGCCAGCTGCAAGAGCCCCCAGATGATGCTGGCGGCCATG
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Pred. No. 0.00
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1393 AACCTGCTGCGCGCCATCGAGGCCCCAGCAGCTGCCTGCAGCTGACCGTGTG 1445
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Search completed: June 8, 2003, 10:17:54
Job time: 857 secs

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Maximum Match 100%
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seq length: 2000000000
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5292.932 Million cell updates/sec
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfIles1.seq:*
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Copyright (c) 1993 - 2003 Compugen
      Length
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           5215881-2
US-09-124-541-3
5244-92-2
US-09-105-537-3
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US-09-103-840A-2
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US-08-804-198-1
US-09-28-517-1
US-09-385-028-19
US-09-385-028-13
US-09-385-028-11
US-09-385-028-11
US-09-385-028-11
US-09-03-287-7
US-09-03-287-7
US-08-510-6468-1
US-08-510-6468-1
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NAME/KEY: CDS LOCATION: 20110	NAME/KEY: CDS LOCATION: 14046 EATURE:	NAME/KEY: CDS LOCATION: .3501400	OGY: linear E TYPE: DNA	nucleic acid	RACTE	; TELECOMMUNICATION INFO	REGISTRATION NUMBER:	; CLASSIFICATION: 433 ; ATTORNEY/AGENT INFORMA : NAME: Plant Thomas	; APPLICATION NUMBER: U	; SOFTWARE: ASCI(DOS) TO CURRENT APPLICATION DATA	; COMPUTER: IBM Compa ; OPERATING SYSTEM: M	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy	ZIP: 46285	i i	ATTITION OF STATE OF	ONDENCE ADI	E OF INVENTION:	Rosteck, F	PLICANT: Ruhstoss	e 7, Application No. 5876991	RESULT 1 US-08-804-227C-7		2.3 346 2.3 346	2 55.8 2.3 151 3 55.2 2.3 44115	40 56 2.3 493 41 55.8 2.3 9	9 56.2 2.3 4 9 56.2 2.3 12	6 56.2 2.3 42 7 56.2 2.3 42	5 56.8 2.4 22 5 56.6 2.4 12	2 56.8 2.4 227 3 56.8 2.4 227	0 57.4 2.4 175 1 57 2.4 99	.8 2.4 1122 .4 2.4 175
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Best Local Similarity 43.5%;
Matches 502; Conservative
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31329..36071
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36155..41830
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US-08-804-198-1
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Patent No. 5945320
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                       TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                       FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: PAUL R. CANTRELL 1:
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROSteck, Paul R., Jr. TITLE OF INVENTION: PLATENOLIDE NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9
TELECOMMUNICATION INFORMATION:
                                                                       FEATURE:
NAME/KEY:
                                   FEATURE
                                                                                                                                                                                                   EATURE:
                                                                                                                                                                                                                  MOLECULE TYPE:
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NAME/KEY:
LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                  LOCATION:
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Kuhstoss, Stuart A.
Rao, Nagaraja R.
Richardson, Mark A.
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Best Local Similarity 43.5%;
Matches 502; Conservative
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      GCGGCGGCCAGCCCCCCCCCCCACCGACAAGGCCATCACGCAGAAGCGGCAGGCGGCGC 1485
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Pred. No. 0.00012;
0; Mismatches 641;
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1217 CGCCGAGGCCGCGCGCACGGCACCCCCGGGCCGCTGGCCTTGGGACGGGACGGCGGCTT 1276
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APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: McDaniel, Robert
IAPPLICANT: McDaniel, Robert
ITILE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
CURRENT APPLICATION NUMBER: Us/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER FILING DATE: 1999-216
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOT: 1998-10-29
NUMBER OF SEQ ID NOT: 1998-10-29
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 1
LENGTH: 50937
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US-09-428-517-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09428517 Patent No. 6251636 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 376; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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                                                  3654 CGTCGAACTCGACGGCCAGGAGCCGTTCGGCCGTCGGCCCTGGGGTCTACGGCGACGTCAG
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GATCGACCGGG----CCGTGTCGATCGCGCGGACGGCGAGGACCGCGGTCGTCTTCGCGTA
                                                                                                       GGCGAAGTCGCCCATGACCTTCGAGCTGACGTGGGTCACTCCGCAGGCCGCCCAGGAGGC
                                                                                                                                                            GCCGCGCCTGAGCCTGAGCGAGGTGCGCGCGATGGACGGCATCAAGGAGACCAACATCAC
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APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding En
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: JACOBSON, PRICE, HOLMAN & STERN
STREET: The Jenifer Buliding, 400 Seventh
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Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: SUBAN
            TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
APPLICATION UNMBER: US 08
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                               NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: The Jeni
CITY: Washington
                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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1182 base pairs
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Best Local Similarity 43.5%;
Matches 475; Conservative
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                                  ACCAGCGAGGACGGCAGGGGCGCCATCACACTGCGCGTGGCCCAACGGGCTGGGC
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Pred. No. 0.00013;
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TELEX: RCA 24853 IDEA UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-385-028-13
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APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Shish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding En:
Patent No. 6232106
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN,
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US-09-385-028-13
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                                                                                                                                                    Query Match
Best Local Similarity
Matches 475; Conserv
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION UNMEER: US 08/790
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
TELEPAX: (202) 39305350
TELEPAX: (202) 39305350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING-SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                          CTGGGCCTGGCGGCGGCCACCACCCCAAGCAGCTGGCCGAGGGCCTCCGCCGCCTC
         GACTTCACCGTCCTCGCCTCCACCGCCCCCGCCACCGTGAGCGCCGTCTTCACCCGCTCC
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ilarity 43.5%;
Conservative
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                                                                                                                                                Score 63.4; DB 4;
Pred. No. 0.00022;
0; Mismatches 586;
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APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding
PATENT NO. 6232106
TITLE OF INVENTION: Acid Binameter
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street,
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APPLICATION NUMBER: US 06
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
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REFERENCE/OOCKET NUMBER: 14.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
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CITY: Washington
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Sequence 11, Application US/09372422A Patent No. 6313375 GENERAL INFORMATION: SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 11 LENGTH: 1217 FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-8-11 PRIOR APPLICATION NUMBER: US 60/098,692 PRIOR FILING DATE: 1998-08-31 NUMBER OF SEQ ID NOS: 49 APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof

1457

8932 1397 8872 1337 8752

1217

1277

8812

1157 8632

8692

8572 1058 8512 8452 938 8395 878

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GENERAL INFORMATION:
APPLICANT: Jayne, Susan
APPLICANT: Barbour, Eric
APPLICANT: Meyer, Terry
TITLE OF INVENTION: METHODS FV
FILE REFERENCE: moPAT_moCAH
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US-09-003-287-7
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; NAME/KEY: CDS
; LOCATION: (01)..(732)
US-09-003-287-7
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CURRENT FILING DATE: 1998-01-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09003287 Patent No. 6096947
                                                                                                                                                                                                                Matches 305;
                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Myrothecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (110)...(974)
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                                                                                                                                                           GGACGCCGACCCCACCCTGCGCCCAGCTGGACCACCATCACCACCCGTGGAGCTGGGCAA
AATGGGCGTGGGCTCGGGCGCGCGGCGTGTTCGGCACCGCCGGCGGTGTCATGGAGGC 1054
                                                                                             CATCTTCAAGGAGCGCGGCATCAACCTGGCCGAGCTGCCCGAGGGCGAGTGGGACAATCC
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                                                          CGCCTTCCCAGCGGCCGACAAGCTCGTGGCCGAGGCCCAGGCGTTCGTCAAGGCCCGCCT
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                              Score 61.8; DB 3;
Pred. No. 0.00024;
0; Mismatches 357;
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Pred. No. 0.00019;
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RESULT 9
US-07-945-283-1/c
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                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RIBANDO; Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: pseudorabies
TITLE OF INVENTION: involving Th
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
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                   TELEFAX: 309-68
INFORMATION FOR SEQ
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                COUNTRY:
ZIP: 616
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                                                                                                                                                                                                                                                                                                                                                                                                                              1815 No.
                                                                                                                                                                                                                                                                                                                                                                     USA
                                      309-685-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andrew K.
Ronald D.
Pseudorables Virus Deletion Mutants
Involving The EPO and LLT Genes
                                                                                                                                                                                                                                                                                                                                                                                                                              5352596th University Street
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                                                                                                                                                                                                                                             Version
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LENGTH: 8438 base pairs
TYPE; NUCLEIC ACID
STRANDEDNESS; double

TOPOLOGY: linear

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; LOCATION:
US-07-945-283-1
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Best Local Similarity 43.1%;
Matches 358; Conservative
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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NAME/KEY:
LOCATION:
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                          ATGGGCGTGGGCTCGGGCGCGCGTGCTTCGGCACCACCGGCGGTGTCATGGAGGCG 1055
                                                          TGGACCGGGCGCCCGACATCGGCCGCCTCAACGCCCAGGGGGTGCTGCTGCTCTCGGCG 3370
                                                                                   ATCTTCAAGGAGCGCGGCATCAACCTGGCCGAGCTGCCCGAGGGGCGAGTGGGACAATCCA 995
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 CTGCTCGCCGCCTTCGCCCACCGCCTCTGCACGCCGGACTCGCACGCCTGGGCCGGGAAC:3430
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Pred. No. 0.00044;
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US-08-403-852D-1
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Sequence 1, Apr-
No. 5891695
                                                                                                                                                                    TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                 FILING DATE: 10-MAY-15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION DATA:
APPLICATION NUMBER: PRIOR APPLICATION DATA:
APPLICATION NUMBER: PRIOR APPLICATION DATA:
APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR DATE: 25-SEP-15
                   MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                              FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/403,85
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TITLE OF INVENTION:
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                                                                                                                                                SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Wash:
STATE: D.C
                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                      TYPE: nucleic
STRANDEDNESS:
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                                                                         TOPOLOGY: linear
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                                                                                                                               LENGTH:
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Polypeptides Involved In The
INVENTION: Biosynthesis Of Streptogramins,
INVENTION: Coding For These Polypeptides A
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                                                                                                                5392 base pairs
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Jacques, Nathalie
Lacroix, Patricia
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Zagorec, Monique
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And Their Use
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Best Local Simi
Matches 496;
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Pred. No. 0.00048;
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RESULT 11
US-08-510-646B-1
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                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION NUMBER: FR 92/11441
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/ACENT INFORMATION:
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                                                                                                        TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
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                                                                                                                                                              NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
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HYPOTHETICAL:
                  MOLECULE TYPE:
                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                  TOPOLOGY:
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ORIGINAL SOURCE:
ORGANISM: S.P
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                                CACCAGCGAGGACGGCAGGGCGCATCACACTGCGCGTGGCCGAACGGGCTGGG 1336
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                                                                                                   TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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TOPOLOGY: 1in
MOLECULE TYPE:
HYPOTHETICAL: 1
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TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins,
TITLE OF INVENTION: Coding for These Polypeptides Ar
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett (
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                             FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9:
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,81
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MEDIUM TYPE: Floppy disk
                                                                                                                                                          REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
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PRIOR APPLICATION DATA:
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CITY: Washington
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ZIP: 20005-3315
                                                                                                                                                                                                              NAME: Meyers, Kenneth REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                   STRANDEDNESS:
                                                                    TYPE: nucleic acid
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Jacques, Nathalie
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GCGCATCGCTGTCACCGGTTCCATCGCCACCGACCATCTGATGGTCTTCCCCGGCC---G
                           CACCAGCGAGGACGGCAGGGGCGCATCACACTGCGCGTGGCCGTGGCCAACGGGCTGGG 1336
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                                                                                        ATGGTGCCCGCGCGCGCCAAGTTTGAGGAGCTGCTGAAGCACCGCGCCG-CCGCGCG 1216
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                                                                                                                                                                             Matches
                                                                                                                                                                                           Query Match 2.5%;
Best Local Similarity 43.2%;
                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 0917

TELECOMMUNICATION INFORMATION: ...

TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/804,439A FILING DATE: February 21, 1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 92037
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E: CA
TRY: USA
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 CACGTCATCACCACCGTGGAGCTGGGCAACATCTTCAAGGAGCGCGGCATCAACCTGGCC
                                    ATCAAGGACAGCGGCCTGCTGGACTACACGGAGGTCCAGCGCGCAACCAGCTGCACGAC
                                                                     TCGGAGGCTGACCGCGACTGGTTCTGTGTGGACGCCGACCCCACCCTGCGCCAGCTGGAC
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                                                                                                                                                                                           Score 61;
Pred. No.
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US-08-720-229-13
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Sequence 13, Appr
Sequence 13, Appr
COUNTRY: USA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Ve
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,229
FILING DATE: 26-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCHIff, J. MICHAE!
REGISTRATION NUMBER: 40,253
REGISTRATION NUMBER: 29938-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) A1-5600
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison &
STREET: 755 Page Mill
                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: CA
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                          29938-20002.00
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RESULT 15
US-09-103-840A-2/c
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; Patent No. 6294328
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPDLOGY: linear
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

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Search completed: June Job time : 2876 secs
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ORGANISM: Mycobacterium tuberculosis

FEATURE:

OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence

OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENCIN Ver. 2.1
SEQ ID NO 2
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Best Local Similarity 48.8%;
Matches 163; Conservative
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/cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
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Sequence 51, Appl
Sequence 200, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 20, Appl
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AT.T CHMENT'S	US-09-860-846-32	US-10-166-087-45		US-09-476-242-13		US-10-166-087-1	-	US-09-861-289-1	US-09-836-821-1	US-09-988-384B-1	US-09-860-846-1	US-09-815-242-7870		US-09-861-289-5	US-09-836-821-5	US-09-860-846-5	US-09-861-289-30	US-09-836-821-30	US-09-988-384B-30	9-860-846-	US-10-126-927-68	•	US-09-476-242-12	-09	-476-242-	US-09-476-242-26
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ALIGNMENTS

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Sequence 3, Application US/09476242
Patent No. US20020146683A1
GENERAL INFORMATION:
APPLICANT: BARNETT, SUSSIN
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 2310
TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-476-242-3
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Best Local Similarity 44.3%;
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                                     642 CCGCTGCCCATGTTCACCAGCTGCTGCCCCGGCTGGATCGCTATGCTGGAGAAATCTTAC
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RESULT 2
US-09-476-242-4
Sequence 4, Application US/09476242
Patent No. US20020146683A1
PAPLICANT: HARTON: SUSAN
APPLICANT: HARTON, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
PILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 4
LENGTH: 2316
TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION:
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                                                OTHER INFORMATION: -09-476-242-4
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RESULT 3
US-09-476-242-8
; Sequence 8, Application US/09476242
; Patent No. US20020146683A1
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan

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APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 199-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 2316
TYPE: DNA
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: BARNETT, SUSAN
APPLICANT: HARTOR, KATIN
APPLICANT: HARTOR, KATIN
APPLICANT: HARTOR, KATIN
APPLICANT: MARTIN, ETIC
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 2322
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: TORGER INFORMATION: Description of Artificial Sequence: Vall20-Ile201B
US-09-476-242-5
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Best Local Similarity 44.3%;
Matches 422; Conservative
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                                   942 AAGGAGCGCGGCATCAACCTGGCCGAGCTGCCCGAGGGGCGAGTGGGACAATCCAATGGGC
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                                                                                  922 CTGTTCAACAGCACCTGGAACAACACCATCGGCCCCAACAACACCAACGGCACCATCACC
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pred. No. 4e-09;
pred. No. 4e-09;
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APPLICANT: BARNETT, SUSAN
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEP
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 2328
TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-476-242-6
; Sequence 6, Application US/09476242
; Patent No. US20020146683A1
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APPLICANT: BARNETT, Susan
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEF
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 199-12-30
NUMBER OF SEQ ID NOS: 26
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-476-242-7
US-09-476-242-7
; Sequence 7, Application US/09476242
; Patent No. US20020146683A1
; Patent No. TONATTON;
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                                                                    ; OTHER INFORMATION:
US-09-476-242-7
Query Match 2.9%;
Best Local Similarity 44.3%;
Matches 422; Conservative
                                                                                                         LENGTH: 2334
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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   Score 69.8; DB 10;
Pred. No. 4e-09;
0; Mismatches 522;
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                                                                                              Artificial Sequence: Leu122-Ser199
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       Indels
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RESULT 7
US-09-476-242-25
   Sequence 25, Application US/09476242
Patent No. US20020146683A1
GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: HARTOG, Karin
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: TITLE OF INVENTION: MODIFIED HIV ENV POL

: FILE REFERENCE: 1605.002

: CURRENT APPLICATION NUMBER: US/09/476,24

: CURRENT FILLING DATE: 1999-12-30

: NUMBER OF SEO ID NOS: 26

: SOFTMARE: Patentin Ver. 2.0

: SEQ ID NO 25

: LENGTH: 2358

: TYPE: DNA

: ORGANISM: Artificial Sequence

: FEATURE:
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CURRENT APPLICATION NUMBER: US/09/808,880
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US/09/428,517
PRIOR APPLICATION NUMBER: US/09/428,517
PRIOR PRILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/120,254
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1998-10-29
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Matches 376; Conserv
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APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
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CACCAGCGAGGACGGCAGGGGCGCATCACACTGCGCGTGGCCGTGGCCAA-----
                                                                        CGACGACGGCTCGGAGGACCGGGACCGCACGTCGCTGTCCCTGCCCGGCCGAGGACGA 3358
                                                                                                                                            CGCCGAGGCCGCCGCGCACGGCACCCCCGGGCCGCTGGCCTGGGACGGCGGCGGGCTT 1276
                                                                                                                                                                                                                        GÁTCGACCGGG----CCGTGTCGÁTCGCGCGGACGGCGACGGACCGCGGTCGTCTTCGCGTA 3418
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45.6%;
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Pred. No. 2.5e-07;
0; Mismatches 419;
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US-10-171-311-51
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                                                                                                                                                                                                                            ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/398,155
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-06-13.
PRIOR PRIOR PRIOR NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEO ID NOS: 238
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                                                                                                                                                                                                                                                                                                    SEQ ID NO 51
                                                                                                                                                    Matches 161;
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Glatt, Karen
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersh, Sebastian
APPLICANT: Hoersh, Sebastian
APPLICANT: Hoersh, Sebastian
APPLICANT: HOESTHOWEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MR.1-035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schlegel, Robert APPLICANT: Chen, Yan APPLICANT: Zhao, Xumei
                                                                                                                                                                                                                                                                                  JENGTH: 15952
                                                                                                                                                                        Local
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                                                                                                          1142 GGAGACCAACATCACCATGGTGCCCGGCCCCGGGTCCAAGTTTGAGGAGCTGCTGAAGCA 1201
                                FastSEQ
                                                                                                                                                h 2.7%;
Similarity 49.8%;
61; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGATCAGCGCCGTGGCCGCGGTCAACCCACGGACCGTGGTGGTGCTCAACACGGGCTC
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GGCCGTGGCCGCGGGCGTGGTGGGCGGCGAGATCCAGGAGAAGCTGCTGTCGGCCGAGCG
                                                                          GCAGGCGGCCACCGGCTTCGTCATCGACCCCGTGCGCAACCTGAGGCTGTCGGTGGAGGA
                                                                                                                                                                                                                                                                                                                            for Windows Version 4.0
                                                                                                                                                  Score 63.8; DB 9;
Pred. No. 3e-07;
0; Mismatches 162;
                                                                                                                                                        162;
                                                                                                                                                                                          Length 15952;
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RESULT 11
US-09-476-242-18
; Sequence 18, Application US/09476242
; Patent No. US20020146683A1
; GENERAL INFORMATION:
; APPLICANT: BARNETT, SUBAN
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US-09-918-995-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
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TITLE OF INVENTION: NOVEL NUCLEIC
TITLE OF INVENTION: FROM VARIOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 44
TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (1)...(447)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                            GACATGCGGATAAGGCCCTGCTGCGGCAGATGGAAGGCATTTACGCTGACATCCCTGTGC
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                                                                                                                                                                                                        GGCGTCCGGAGTCCAGTGCACGTGCAGGAGCTGTACCAGGAGTGGCTGGAGGGGATCA
                                                                                                                                                                                                                                        GCCGCAGCCAGAACCCGTCCATCCGCGAGCTGTACGACACGTACCTCGGAGAGCCGC 1575
                                                                                                                                                                                                                                                                                                           AGGCCATCACGCAGAAGCGGCAGGCGGCGCTGTACAACCTGGACGAGAAGTCCACGCTGC 1515
                                                                                                                                                                                                                                                                                                                                                                                                               GAÑACATCCAGAÂCATGATCCTGAAGCTTAAGAAGGCAAGTTCCCATTCCACTTTGTGG
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Pred. No. 1.3e-07;
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SEO ID NO 18
LENGTH: 2322
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 43.9%;
Matches 417; Conservative
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APPLICANT: MARTIN, EFIC
TITLE OF INVENTION: MODIFIED HIV ENV POLYI
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
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                GTGGCCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTG
                                          GACGGCGGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGCGACATG
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Sequence 10, Application US/09476242
PARENT NO. US20020146683A1.
GENERAL INFORMATION:
APPLICANT: BARRETT, Susan
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEP
FILE REFERENCE: 1605.002
CURRENT APPLICATION UMMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
LENGTH: 2541
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US-09-476-242-10
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US-09-476-242-22
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US-09-476-242-22
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CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 2298
TYPE: DNA
ORGANISM: Artificial Sequence
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Patent No. US20020146683A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 426;
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Best Local Similarity 44.5%;
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APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV
FILE REFERENCE: 1605.002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62.6; DB 10;
Pred. No. 3.7e-07;
0; Mismatches 519;
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Sequence 23, Application US/09476242

Patent No. US20020146683A1

GENERAL INFORMATION:

APPLICANT: HARTOG, Karin

APPLICANT: HARTOG, Karin

APPLICANT: HARTOG, Karin

CITTLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES

FILE REFERENCE: 1605.002

CURRENT APPLICATION NUMBER: US/09/476,242

CURRENT FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 23

LENGTH: 2298

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: Val120-Ile201B; Ile424-Ala433

US-09-476-242-23
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RESULT 15 US-09-476-242-24 ; Sequence 24, Application US/09476242 ; Patent No. US20020146683A1

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GENERAL INFORMATION:
APPLICANT: BARNETT, SUBBIN
APPLICANT: HARTOG, KARÍN
APPLICANT: MARTOG, ERÍC
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 199-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 24
LENGTH: 2298
LENGTH: 2298
TYPE: DNA
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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vall20-Thr202;
; OTHER INFORMATION: Ile424-Ala433
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Search completed: June 8, 2003, 14:36:16 Job time: 383 secs

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ALIGNMENTS

FEATURES source		JOURNAL	TITLE	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BI717904 LOCUS DEFINITION
Email: Chauser@duke.edu. Location/Qualifiers 1657 /organism="Chlamydomonas reinhardtii"	DCMB Box 91000 Duke University Durham, NC 27708-1000 Tel: 919 613 8159 Fax: 919 613 8177	Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031 Unpublished (2001) Contact: Charles Hauser	Grossman, A., Chang, CW., Dayles, J., Harris, E., Hauser, C., Letebyre, P., McDermott, J. P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model,	Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas. 1 (bases 1 to 657)	Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. B1717904 B1717904.1 GI:15693599 EST. Chlamydomonas reinhardtii.	BI717904 657 bp mRNA linear EST 19-SEP-2001 1031022F12.y1 C. reinhardtii CC-1690, Stress II (normalized),

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Query Match
Best Local
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/db_xref="taxon:3055"
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Unpublished (2001)
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DCMB Box 91000
Duke University
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TTGCGCGGCTGCCGCACCCGCTGCGGAGGCGCCTTTGAGTCATGTCCAGCAGGCGCTCGC
                                      CACCGTGCGTGTAGCCCTTGCAACACTTGAGGGGCCCCGCACGCCCTAGGCAACGTCGC 316
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Pred. No. 4.5e-119;
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source /organism="CC-1690 wild type mt+ 21gr" /strain="CC-1690 wild type mt+ 21gr" /db_xref="taxon:3055" /db_xref="taxon:3055" /clone lib="C. reinhardtii CC-1690, Stress II (normalized) /clone lib="C. reinhardtii CC-1690, Stress II (normalized) / Lambda Zap II" /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II sk-ary, constructed by John- Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). POLYA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome	Tel: 919 613 8197 Fax: 919 613 8177 Email: chauser@duke.edu. FEATURES FEATURES FEATURES	Vascular Plants. Project: 1031 JOURNAL Unpublished (2001) COMMENT Contact: Charles Hauser DCMB Box 91000 DCMB Box 91000 Duke University Duke University	REFERENCE 1 (bases 1 to 644) AUTHORS Grossman,A., Chang,CW., Davies,J., Harris,E., Hauser,C., Lefebvre, P., McDermott,J.P., Shrager,J., Sifflow,C. and Stern,D. TITLE Analyses of the Chlamydomonas reinhardti Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in	WSI	LOCUS EM003317 644 bp mRNA linear EST 25-OCT-2001 DEFINITION 1031109G06.yl C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. ACCESSION EM003317 VERSION EM003317 GI-16438097	т 3 317	OY 617 GGAGGCCCACCCGCACTCCGACGACGCCGCTGCCCATGTTCACCAGCTG 664	Qy 557 CGCCGACCTGACCATCATGGAGGAGGGAGGGAGCTGCTGCACCGCCTCACCGAGCACCT 616	Qy 497 GCAGCTGGCCGAGGGCCTCCGCCCTCGGCTTTGACGAGGTGTTTGACACGCTGTTTGG 556	Qy 437 GGCCGTTCGTGTCGCTATTGCCGAGACCCTGGGCCTGGCGCCGGCGGCGCCACCACCACCCCCAA 496	QY 377 CGAGCTTGCCAAGGACGACGACGACGCCAAGGACGTCTGCGTGCAGGTGGCTCC 436	Db . 301 TTGCGCGCCACCCGCTGCGGAGGCGCTTTGAGTCATGTCCAGCAGGCGCTCGC 360
RESULT 4 B1716102 B1716102 B1716102 B1716102 B1716102 B1716102 B1716102 Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. ACCESSION B1716102 VERSION B1716102.1 GI:15691797 EST. SOURCE Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadsceae; Chlamydomonas AUTHORS P., McDermott, J.P., Shrager, J., Harris, E., Hauser, C., Lefebvre Unicellular System for Analyzing Gene Function and Regulation in Unpublished (2001) COMMENT CMM BOX 91000	OY 1355 CACCAAGATGCAGGCCGAGGCCAAGTACGACTTT 1391	Db 488 CGGCACCCCCGGGCCGCTGGCCTGGACGGCGGGCGTTCACCAGCGAGGACGGCAG 547 Oy 1295 GGGCGCATCACACTGCGCGTGGCCATGGCCAACGGCTGGGCAACAACAACCTGAT 1354	1175 GTCCAAGTTTGAGGAGCTGCTGAAGCACCGCGCGCCGCGCGCG	OY 1115 CGAGGTGCGGGGATGGACGGCATCAAGGAGACCAACATCACCATGGTGCCCGCGCCCGG 1174	OY 1055 GGCGCTGCGCACGGCCTATGAGGTGTTCACGGGCACGCCGCGCGCG	OY 995 AATGGGCGTGGGCTGGGCGCGGCGTGTTTCGGCACCGGCGGTGTCATGGAGGC 1054	QY 935 CATCTTCAAGGAGGGGGGATCAACCTGGCCGAGGGCCGAGGGGGAGTGGGACAATCC 994	QY 875 GGACGCGACCCCTGCGCCAGCTGGACCACGTCATCACCACCGTGGAGCTGGGCAA 934	OY 815 GGTGTCCATCATGCCCTGCACGCGCAAGCAGTCGGAGGCTGACCGCGACTGGTTCTGTGT 874	OY 755 GGCCATGGTCAAGTCCTACCTAGCGGAAAAGAAGGGCATCGCGCCAAAGGACATGGTCAT 814	Query Match 26.6%; Score 637; DB 13; Length 644; Best Local Similarity 100.0%; Pred. No. 5.4e-119; Matches 637; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	BASE COUNT 118 a 213 c 230 g 83 t ORIGIN

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Durham, NC 27708-1
Tel: 919 613 8159
Fax: 919 613 8177
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CGCCGACCTGACCATCATGGAGGGAGGGCAGCGAGCTGCTGCACCGACCCTCACCGAGCACCT
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/ LamEda Zap II"
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Matches 614; Conserv
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EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                            61
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Grossman.A., Chang.C.-W., Davies,J., Harris,E., Hauser,C., Lef Grossman.A., Chang.C.-W., Davies,J., Silflow,C. and Stern.D., P., McDermott,J.P., Shrager,J., Silflow,C. and Stern.D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation Unicellular System for Analyzing Gene Function and Regulation
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Unpublished (2001)
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Tel: 919 613 8159
Fax: 919 613 8177
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DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: chauser@duke.edu.
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                                                                                                                                                                                                                                                                                                                       xhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines CDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4 - containing) and shifted to TAP - NO3 - (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + Sorbitol (1, 2, 6, 24 hr); TAP + H2O2 (1, 12, 6, 24 hr). Polya mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda your sizes. PBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="CC-1690 wild type mt+ 21gr"
/db xref="taxon:3055"
/clone lib="C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II"
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Pred. No. 4.3e-114;
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EST.
Chlamydomonas I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 bp mRNA linear EST 894076B10.yl C. reinhardtii CC-1690, normalized, Lambda Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
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Unpublished (2000)
Contact: Charles Hauser
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                                                                                                                                                                                    B Box 91000
e University
ham, NC 27708-1000
: 919 613 8159
: 919 613 8179
                                                                                                                                                                          chauser@duke.edu
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-tog phase in TAP (acetate-containing) medium in the
                                                                          /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, nc
                                                                                                                                                          Location/Qualifiers
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ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and xhol (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT
98 a 225 c 169 g 107 t 2 others

ORIGIN

Query Match
24.9%; Score 596.4; DB 12; Length 601;
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                                     Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota, Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 558)
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         Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433
                                                                                                AV389547.1
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AV389547 Chlamydomonas
cDNA clone CM044d10_r,
AV389547
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20152988
Contact: Yasukazu Nakamura
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1024021E05.yl (
Chlamydomonas )
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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/clone="CN044d10 r"
/clone_li="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_l:
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Pred. No. 1.1e-102;
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Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation
Vascular Plants; project phase 2
Unpublished (2000)
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ATACGACAACGGGGCCCGTGAGGATTGAGCACTTGACTCGCGAACTTATGAACGTAGCGC
                         ATACGACAACGGGGCCCGTGAGGATTGAGCACTTGACTCGCGAACTTATGAACGTAGCGC 2219
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milarity 95.7%; P
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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Pred. No. 2.4e-100;
0; Mismatches 25;
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/note="Ve XhoI; Thi McDermott	1 CGGCATCACACTGCGCCGTGGCCCAACGGGCTGGGCAACGCCAAGAAGCTGATCAC	Db 4
/clone_li	1298 CGGCATCACACTGCGCGTGGCCGTGGCCAACGGGCTGGCCAACGCCAAGGAACCTGATCAC 13	Ş
/organism /strain=" /db xref=	Matches 545; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Best Mate
FEATURES Location source 1621	, , , , , , , , , , , , , , , , , , ,	ORIGIA
Fax: 919 613 8177 Email: chauser@duk		BASE
Duke University Durham, NC 27708- Tol. 010 613 0150	ramuda AAF CIONES DY SUBERINIECTION WITH EXASSISC (Stratagene) phage. The library was normalized using method 4 described in Renaldo er al (1996) Genome	
DCMB BOX 91000	sites pluescripte, in the state and show the	
PL.	sorty many was purified from each sample, pooled and chwa synthesized. The cDNA was directionally cloned into lambda	
Unicellular System	Solid TANA TO THE FIRST TAP F CD (1, 2, 11) THE F	
McDermott, J	conditions (0 12hr, 204) see Melis et al. (200) Plant	
1 (bases 1	cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP . NO3- (24hre): H2 production	
OKGANISM Chlamydomonas rei Chlamydomonadacoa Chlamydomonadacoa	Notes vector: paruescript i sky, site i: Ecoki; site 2: Xhoī, Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines chuke from CC-1690	
?), Lambda Zap II"	
	/db_xref="taxon:3055" /clone lib="C. reinhardtii CC-1690. Stress II (normalized	
Chlamydomonas rein	<pre>/organism="Chlamydomonas reinhardtii" /strain="CC-1690 wild type mt+ 21qr"</pre>	
DEFINITION 1024021E05.x2 C.	source 1599	
BG848384/c	Email: ch	PE ATTIPES
RESULT 10	Fax: 919 613 8177	
טאו אפווטרר פאי	Durham, NC 27708-1000	
	DCMB Box 91000	
Qy 1838 AGTAGGC 1844	è	COMMENT
Db 481 GGCGGGTCAAATGTTT	Vascular Plants. Project: 1031	101
Qy 1778 GGCGGGTCAAATGTT	TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in	TITI
Db 421 AATATGCACTGATGG	AUTHORS · Grossman,A., Chang,CW., Davies,J., Harris,E., Hauser,C., Lefebvre	AUTI
Qy 1718 AATATGCACTGATGGG		REFERI
361	MELEN	SOURCE
1658	VERSION BI716925.1 GI:15692620 KEYWORDS EST.	VERSION
101 CTTCACACACACACACACACACACACACACACACACACA	Lambda Zap II Chlamydomonas reinhardtii cDNA, m	ACCES
1 1	ź	LOCUS
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18.00		
Db 181 GCCGCCCTGTACAA		D 5
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Oy 1418 CTGTGTGGGCGGCGGC Db 121 CTGTGTGGGCGGCGGC	2280 AGATGCATTGCAAACGCCTGTAAAAGAACGGCATAGCTACTAGACACTCTGATGTGGACC 2339	B 8
Db 61 CAAGATGCAGGCCGGC	438 TTTATACCCACCGTATGCGATTGACGTTGGTGTAGGTAACCAGGCGGTAGGAAGGCGGAG 497	מט
1358	TTTATACCCACCGTATGCGATTGACGTTGGTGTAGGCAACCAGGCGGTAGGAAGGCGGAG	ş Ş
)

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/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells,grown to
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                                                                   mm="Chlamydomonas reinhardtii"
:"CC-1690 wild type mt+ 21gr"
:="taxon:3055"
ib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                             ike.edu.
i/Qualifiers
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Iplantae; Chlorophyta; Chlorophyceae; Volvocales;
me; Chlamydomonas.
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reinhardtii CC-1690, normalized, Lambda Zap II
.nhardtii cDNA, mRNA sequence.
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                               AV396217

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N AV396217

AV396217

AV396217.1 GI:6550433

EST:

Chlamydomonas reinhardtii.

Chlamydomonas reinhardtii.

SM Chlamydomonas reinhardtii

Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Viridiplantae; Chlorophyta; Chlamydomonadaceae; Chlamydomonas.
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samizu, E., Nakamura, Y.,
large scale structural
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Pred. No. 2.7e-99;
0; Mismatches 37;
Sato,S., Fukuzawa,H. and Tabata,S. analysis of cDNAs in a unicellular
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ORGANISM

Chlamydomonas reinhardtii Chlamydomonas reinhardtii

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AV396237
AV396237 Chlamydomonas reinhardtii C9 Chlamydomonas CDNA clone CL58a12 r 5', mRNA sequence.

EST 23-APR-2002 reinhardtii

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non-redundant expressed
DNA Res. 6 (6), 369-373 (1999)
E 20152088
Contact: Yasukazu Nakamura
The First Laboratory for Plant Ge
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292
Email: ynakamu@kazusa.or.jp, URL
Location/Qualifiers
538
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                       CCGAGGGCCTCCGCCGCCTCGGCTTTGACGAGGTGTTTGACACGCTGTTTTGGCGCCCGA
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/db_xref="taxon:3055"
/clone="CL58b09_r"
/clone_1b="Chlamydomonas rein
/dev_stage="photoautotrophic g
/dev_stage="photoautotrophic g
/note="Vector: pBluescriptII S
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Pred. No. 1.3e-98;
0; Mismatches 1
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URL:http://www.kazusa.or.jp/en/plant/.
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AV386674 Chlamydomonas reinhardrii C9 Chlamydomonas cDNA clone CM004a11_r, mRNA sequence.
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
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/clone="CL58a12_r"
/clone_lib="Chlamydomonas reinhardtii
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Asamiru, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. Asamiru, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. Alarge scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 29
Email: ynakamu@kazusa.or.jp, UR
Location/Qualifiers
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/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1:
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Unpublished (2001)
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Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Tel: 919 613 8159
Fax: 919 613 8177
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DCMB Box 91000
Duke University
                                                                                                                                                                                                                                                                                                      GGCATTAGGCGTAGGTACTGGCATGAGGGAGCGCGGCTTGCTAACCGAATGGCGTATCCC 1919
                                                                                                                                                                                          TCCAGGGCACGTCGGAATGGCGCGTGCCCATCAACGCAAATTCTTGGCCTTCATCGCTTC 1979
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       GGTTGGAAGCTAAACATGTTTGGGAACAATTCATCTTACTAAAGCGTGTGGGGGGTTGAGG 2099
                                                                                 TGGATATTGAAGCTGCACAAACCTGCATTCTATTTGCTTGTTTACACGTGCCCCAATCTT 2039
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                                                       TGGATATTGAAGCTGCACAAACCTGCATTCTATTTGCTTGTTTACACGTGCCCCAATCTT
                                                                                                                                                          TCCAGGGCACGTCGGAATGGCGCGTGCCCATCAACGCAAATTCTTGGCCTTCATCGCTTC 343
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/db xref="taxon:3055"
/clone lib="C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II"
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Pred. No. 1.1e-86;
0; Mismatches 24; Indels 0;
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Best Local Similarity
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Unpublished (2001)
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Chlamydomonadaceae; Chlamydomonas.
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BI532214.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
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                                                                                                           inotes "Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK. plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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                         19.8%;
      Score 476; DB 13;
Pred. No. 2.3e-86;
0; Mismatches 25;
                                                Length 631;
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